

C. Kaufman

#13

1646

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/096,500A  
DATE: 07/18/2000  
TIME: 13:35:55  
Input Set : A:\P1110P1.txt  
Output Set: N:\CRF3\07182000\I096500A.raw

ENTERED p.5

RECEIVED

AUG 02 2000

TECH CENTER 1600/2900

3 <110> APPLICANT: Ashkenazi, Avi J.  
4 Baker, Kevin P.  
5 Chuntharapai, Anan  
6 Gurney, Austin  
7 Kim, Kyung Jin  
8 Wood, William I.  
10 <120> TITLE OF INVENTION: Apo-2DcR  
12 <130> FILE REFERENCE: P1110P1  
14 <140> CURRENT APPLICATION NUMBER: US 09/096,500A  
15 <141> CURRENT FILING DATE: 1998-06-12  
17 <150> PRIOR APPLICATION NUMBER: US 60/049,911  
18 <151> PRIOR FILING DATE: 1997-06-18  
20 <160> NUMBER OF SEQ ID NOS: 17  
22 <210> SEQ ID NO: 1  
23 <211> LENGTH: 259  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
27 <400> SEQUENCE: 1  
28 Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val 15  
29 1 5 10  
31 Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg 30  
32 20 25  
34 Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg 45  
35 35 40  
37 His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser 60  
38 50 55  
40 Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr 75  
41 65 70  
43 Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val 90  
44 80 85  
46 Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg 105  
47 95 100  
49 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn 120  
50 110 115  
52 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu 135  
53 125 130  
55 Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val 150  
56 140 145  
58 Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu 165  
59 155 160  
61 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu 180  
62 170 175  
64 Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu 195  
65 185 190  
67 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu 210  
68 200 205  
70 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu

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```

71          215          220          225
73 Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
74          230          235          240
76 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
77          245          250          255
79 Ile Val Phe Val
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 1180
84 <212> TYPE: DNA
85 <213> ORGANISM: Homo sapiens
87 <220> FEATURE:
88 <221> NAME/KEY: CDS
89 <222> LOCATION: (193) . . . (969)
90 <223> OTHER INFORMATION:
92 <400> SEQUENCE: 2
93 gctgtgggaa cctctccacg cgcacgaact cagccaacga tttctgatag 50
95 atttttggga gtttgaccag agatgcaagg ggtgaaggag cgcttcctac 100
97 cgtttagggaa ctctggggac agagcgcccc ggccgcctga tggccgaggc 150
99 aggggtgcgac ccaggaccca ggacggcgtc gggaaccata cc atg 195
100                                     Met
101                                     1
103 gcc cgg atc ccc aag acc cta aag ttc gtc gtc gtc atc 234
104 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
105          5          10
107 gtc gcg gtc ctg ctg cca gtc cta gct tac tot gcc acc 273
108 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
109 15          20          25
111 act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 312
112 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
113          30          35          40
115 cca cag caa cag agg cac agc ttc aag ggg gag gag tgt 351
116 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
117          45          50
119 cca gca gga tot cat aga tca gaa cat act gga gcc tgt 390
120 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
121          55          60          65
123 aac ccg tgc aca gag ggt gtg gat tac acc aac gct tcc 429
124 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
125          70          75
127 aac aat gaa cct tct tgc ttc cca tgt aca gtt tgt aaa 468
128 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys
129          80          85          90
131 tca gat caa aaa cat aaa agt tcc tgc acc atg acc aga 507
132 Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
133          95          100          105
135 gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat 546
136 Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn
137          110          115
139 gaa aac tcc cca gag atg tgc cgg aag tgt agc agg tgc 585

```

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```

140 Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys
141      120      125      130
143 cct agt ggg gaa gtc caa gtc agt aat tgt acg tcc tgg 624
144 Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp
145      135      140
147 gat gat atc cag tgt gtt gaa gaa ttt ggt gcc aat gcc 663
148 Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala
149      145      150      155
151 act gtg gaa acc cca gct gct gaa gag aca atg aac acc 702
152 Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr
153      160      165      170
155 agc ccg ggg act cct gcc cca gct gct gaa gag aca atg 741
156 Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met
157      175      180
159 aac acc agc cca ggg act cct gcc cca gct gct gaa gag 780
160 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu
161      185      190      195
163 aca atg acc acc agc ccg ggg act cct gcc cca gct gct 819
164 Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala
165      200      205
167 gaa gag aca atg acc acc agc ccg ggg act cct gcc cca 858
168 Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro
169      210      215      220
171 gct gct gaa gag aca atg acc acc agc ccg ggg act cct 897
172 Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro
173      225      230      235
175 gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 936
176 Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
177      240      245
179 ata gtt cta att gtg ctt ctg att gtg ttt gtt t 970
180 Ile Val Leu Ile Val Leu Ile Val Phe Val
181      250      255      259
W--> 181 gaaagacttc actgtggaag aaattccttc cttacctgaa aggttcaggt 1020
183 aggcgctggc tgagggcggg gggcgctgga cactctctgc cctgcctccc 1070
185 tctgtgtgtg tcccacagac agaaacgcct gccctgccc caaaaaaaaaa 1120
187 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1170
189 aaaaaaaaaa 1180
191 <210> SEQ ID NO: 3
193 <211> LENGTH: 299
194 <212> TYPE: PRT
195 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 3
199 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
200      1      5      10      15
202 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
203      20      25      30
205 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
206      35      40      45
208 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro

```

209					50					55						60
211	Val	Leu	Ala	Tyr	Ser	Ala	Thr	Thr	Ala	Arg	Gln	Glu	Glu	Val	Pro	
212					65					70						75
214	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Gln	Arg	His	Ser	Phe	Lys	Gly	
215					80					85						90
217	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser	Glu	His	Thr	Gly	Ala	
218					95					100						105
220	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr	Thr	Asn	Ala	Ser	Asn	
221					110					115						120
223	Asn	Glu	Pro	Ser	Cys	Phe	Pro	Cys	Thr	Val	Cys	Lys	Ser	Asp	Gln	
224					125					130						135
226	Lys	His	Lys	Ser	Ser	Cys	Thr	Met	Thr	Arg	Asp	Thr	Val	Cys	Gln	
227					140					145						150
229	Cys	Lys	Glu	Gly	Thr	Phe	Arg	Asn	Glu	Asn	Ser	Pro	Glu	Met	Cys	
230					155					160						165
232	Arg	Lys	Cys	Ser	Arg	Cys	Pro	Ser	Gly	Glu	Val	Gln	Val	Ser	Asn	
233					170					175						180
235	Cys	Thr	Ser	Trp	Asp	Asp	Ile	Gln	Cys	Val	Glu	Glu	Phe	Gly	Ala	
236					185					190						195
238	Asn	Ala	Thr	Val	Glu	Thr	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
239					200					205						210
241	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Asn	Thr	
242					215					220						225
244	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
245					230					235						240
247	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
248					245					250						255
250	Ser	Pro	Gly	Thr	Pro	Ala	Pro	Ala	Ala	Glu	Glu	Thr	Met	Thr	Thr	
251					260					265						270
253	Ser	Pro	Gly	Thr	Pro	Ala	Ser	Ser	His	Tyr	Leu	Ser	Cys	Thr	Ile	
254					275					280						285
256	Val	Gly	Ile	Ile	Val	Leu	Ile	Val	Leu	Leu	Ile	Val	Phe	Val		
257					290					295						
259	<210> SEQ ID NO: 4															
260	<211> LENGTH: 1180															
261	<212> TYPE: DNA															
262	<213> ORGANISM: Homo sapiens															
264	<220> FEATURE:															
265	<221> NAME/KEY															

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```

279                                     -40                                     -35
281  cgc ttc cta ccg tta ggg aac tct ggg gac aga gcg ccc 129
282  Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp Arg Ala Pro
283                                     -30                                     -25
285  cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 168
286  Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
287  -20                                     -15                                     -10
289  cag gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc 207
290  Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
291  -5                                     1                                     5
293  aag acc cta aag ttc gtc gtc gtc atc gtc gcg gtc ctg 246
294  Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu
295  10                                     15
297  ctg cca gtc cta gct tac tct gcc acc act gcc cgg cag 285
298  Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln
299  20                                     25                                     30
301  gag gaa gtt ccc cag cag aca gtg gcc cca cag caa cag 324
302  Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln
303  35                                     40
305  agg cac agc ttc aag ggg gag gag tgt cca gca gga tct 363
306  Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser
307  45                                     50                                     55
309  cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca 402
310  His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr
311  60                                     65                                     70
313  gag ggt gtg gat tac acc aac gct tcc aac aat gaa cct 441
314  Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro
315  75                                     80
317  tct tgc ttc cca tgt aca gtt tgt aaa tca gat caa aaa 480
318  Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln Lys
319  85                                     90                                     95
321  cat aaa agt tcc tgc acc atg acc aga gac aca gtg tgt 519
322  His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys
323  100                                     105
325  cag tgt aaa gaa ggc acc ttc cgg aat gaa aac tcc cca 558
326  Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro
327  110                                     115                                     120
329  gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa 597
330  Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
331  125                                     130                                     135
333  gtc caa gtc agt aat tgt acg tcc tgg gat gat atc cag 636
334  Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln
335  140                                     145
337  tgt gtt gaa gaa ttt ggt gcc aat gcc act gtg gaa acc 675
338  Cys Val Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr
339  150                                     155                                     160
341  cca gct gct gaa gag aca atg aac acc agc ccg ggg act 714
342  Pro Ala Ala Glu Glu Thr Met Asn Thr Ser Pro Gly Thr
343  165                                     170

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 07/18/2000

PATENT APPLICATION: US/09/096,500A

TIME: 13:35:56

Input Set : A:\P1110P1.txt

Output Set: N:\CRF3\07182000\I096500A.raw

L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2  
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4  
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11